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Pending Claims

1. A DNA sequence comprising as operably joined components in the direction of transcription, a cotton fiber transcriptional initiation region functional in a cotton fiber cell and an open reading frame encoding a protein in a pigment biosynthesis pathway, wherein said transcriptional initiation region is selected from the group consisting of:
 - a. nucleotides 65-4163 of SEQ ID NO: 7, and
 - b. SEQ ID NO: 15.
2. The DNA sequence according to Claim 1, further comprising a sequence encoding a transit peptide from a plant nuclear-encoded gene.
3. The DNA sequence according to Claim 2, wherein said transit peptide is a plastid transit peptide.
4. The DNA sequence according to Claim 1, wherein said DNA sequence further comprises as an operably joined component a sequence encoding a signal peptide which provides for transport across the rough endoplasmic reticulum.
5. The DNA sequence according to Claim 4, wherein said DNA sequence further comprises as an operably joined component, 3' to said open reading frame, a sequence encoding a vacuolar targeting signal.
6. The DNA sequence of Claim 1 wherein said pigment is melanin or indigo.
7. The DNA sequence of Claim 1 wherein said open reading frame is from a bacterial or a plant gene.
8. The DNA sequence of Claim 7 wherein said gene is selected from the group consisting of ORF438, tyrA, anthocyanin R gene, anthocyanin C1 gene, pig, and tna.

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9. A DNA construct comprising a DNA sequence of Claim 1.
10. A DNA construct comprising a first and a second DNA sequence according to Claim 1, wherein the open reading frame of said first DNA sequence encodes a different protein than the open reading frame of said second DNA sequence.
12. A plant cell comprising the DNA construct of Claim 9.
13. A plant comprising the cell of Claim 12.
14. A method of modifying fiber color in a cotton plant, said method comprising:
transforming a plant cell with a DNA construct comprising a DNA sequence comprising i) a sequence selected from the group consisting of SEQ ID NO:15 and nucleotides 65-4163 of SEQ ID NO:7, and ii) an open reading frame encoding a protein selected from the group consisting of tyrosinase, tryptophanase and indole oxygenase ;
and
regenerating a plant comprising fiber tissue from said plant cell, wherein said fiber tissue comprises a substrate of said protein , and wherein said protein reacts with said substrate to produce a pigment, whereby the color of said fiber is modified.
15. The method of Claim 14 wherein said DNA construct further comprises a sequence encoding a transit peptide from a plant nuclear-encoded gene.
16. The method of Claim 14 wherein said DNA construct further comprises a sequence encoding a signal peptide which provides for transport across the rough endoplasmic reticulum.
18. The method of Claim 16 wherein said plant cell is further transformed with a second DNA construct according to Claim 9 or 10 and wherein the open reading frame of

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the DNA sequence from the first DNA construct encodes a different protein than the open reading frame of the second DNA construct.

19. The method of Claim 18 wherein said pigment is melanin and said proteins are encoded by tyrA and ORF438.

20. The method of Claim 18 wherein said pigment is indigo and said proteins are encoded by tna and pig.

21. The method of Claim 18 wherein said pigment is anthocyanin and said two proteins are the anthocyanin R and C1 proteins.

22. The method of Claim 14 wherein said fiber tissue is obtained from a cotton burr.

23. A recombinant DNA construct comprising nucleotides 65 – 4163 of SEQ ID NO: 7.

24. A recombinant DNA construct comprising SEQ ID NO: 15.

25. An isolated DNA sequence comprising the sequence shown in SEQ ID NO: 1.

26. An isolated DNA sequence comprising the sequence shown in SEQ ID NO: 12.

28. The DNA sequence according to Claim 1, wherein said transcriptional initiation region is obtained by probing a genomic library derived from a plant fiber tissue.

30. The DNA sequence according to Claim 59, further comprising a sequence encoding a transit peptide from a plant nuclear-encoded gene.

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31. The DNA sequence according to Claim 30, wherein said transit peptide is a plastid transit peptide.
32. The DNA sequence according to Claim 59, further comprising a sequence encoding a signal peptide which provides for transport across the rough endoplasmic reticulum.
33. The DNA sequence according to Claim 32, wherein said sequence further comprises, 3' to said open reading frame, a sequence encoding a vacuolar targeting signal.
34. The DNA sequence of Claim 57 wherein said open reading frame is from a bacterial gene.
35. The DNA sequence of Claim 34 wherein said bacterial gene is selected from the group consisting of ORF438, tyrA, pig and tna.
36. A DNA construct comprising the DNA sequence of Claim 59.
37. The DNA construct of Claim 36 wherein said cotton plant cell is a cotton fiber cell.
38. A plant cell comprising the DNA construct of Claim 36.
39. A plant comprising the plant cell of Claim 38.
42. The DNA sequence according to Claim 59 wherein said transcriptional initiation region is obtained by probing a genomic library derived from a plant fiber tissue.
44. A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional initiation region functional in a cotton plant cell and an

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open reading frame encoding an enzyme in a biosynthetic pathway of melanin or indigo, wherein said transcriptional initiation region is selected from the group consisting of:

- a. nucleotides 65-4163 of SEQ ID NO: 7, and
- b. SEQ ID NO: 15.

45. The DNA sequence according to Claim 44, further comprising a sequence encoding a transit peptide from a plant nuclear-encoded gene.

46. The DNA sequence according to Claim 45, wherein said transit peptide is a plastid transit peptide.

47. The DNA sequence according to Claim 44, further comprising a sequence encoding a signal peptide which provides for transport across the rough endoplasmic reticulum.

48. The DNA sequence according to Claim 47, wherein said sequence further comprises, 3' to said open reading frame, a sequence encoding vacuolar targeting signal.

49. The DNA sequence of Claim 44 wherein said open reading frame is from a bacterial gene.

50. The DNA sequence of Claim 49 wherein said bacterial gene is selected from the group consisting of ORF438, tyrA, pig, and tna.

51. The DNA construct comprising the DNA sequence of Claim 44.

52. The DNA construct of Claim 51 wherein said cotton plant cell is a cotton fiber cell.

53. A plant cell comprising the DNA construct of Claim 51.

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54. A plant comprising the plant cell of Claim 53.
55. The DNA sequence according to Claim 44 wherein said transcriptional initiation region is obtained by probing a genomic library derived from a plant fiber tissue.
57. A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional initiation region functional in a cotton fiber cell and an open reading frame encoding an enzyme in the biosynthetic pathway of a pigment, wherein said transcriptional initiation region is selected from the group consisting of:
- a. nucleotides 65-4163 of SEQ ID NO: 7, and
 - b. SEQ ID NO: 15.
59. A DNA sequence comprising a transcriptional initiation region functional in a cotton plant cell, wherein said transcriptional initiation region is selected from the group consisting of:
- a. nucleotides 65-4163 of SEQ ID NO: 7, and
 - b. SEQ ID NO: 15.
65. An isolated DNA sequence comprising nucleotides 65 – 4163 of SEQ ID NO: 7.
66. An isolated DNA sequence comprising SEQ ID NO: 15.
67. An isolated nucleic acid sequence comprising a polynucleotide sequence encoding the polypeptide sequence set forth in SEQ ID NO: 2.
68. An isolated nucleic acid sequence comprising a polynucleotide sequence encoding the polypeptide sequence set forth in SEQ ID NO: 13.